STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 131976

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Wednesday, September 15, 2004
Case Serial Number: 10/018497

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

STIC-Biotech/ChemLib 131976 mej

From: Schultz, James
Sent: Wednesday, September 08, 2004 1:50 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/018,497

Hello,
Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?
Thanks,
Doug Schultz

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
(Office) REM 2D18
(Mail) REM 2C18
(571) 272-0763

****
STAFF USE ONLY

Searcher:_____
Searcher Phone: 2-
Date Searcher Picked up:___
Date Completed: 9/15
Searcher Prep/Rev. Time:___
Online Time:_____

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Type of Search
NA Sequence: #_____
AA Sequence :#_____
Structure: #_____
Bibliographic:_____
Litigation:_____
Patent Family:_____
Other:_____

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other(Specify):_____

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 13:29:27 ; Search time 5963 Seconds
(without alignments)
11215.546 Million cell updates/sec

Title: US-10-018-497A-1
Perfect score: 1543
Sequence: 1 gaattcggatgggctgcacg.....tgaaaaaaaaagccgaattc 1543

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1237800

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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38: em_sy:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1		26	1.7	26	6	I46576	I46576 Sequence 55
2		26	1.7	26	6	I46581	I46581 Sequence 56
3		26	1.7	26	6	I46686	I46686 Sequence 66
4		24.4	1.6	26	6	I46693	I46693 Sequence 67
5		22	1.4	22	6	I46548	I46548 Sequence 52
6		22	1.4	22	6	I46562	I46562 Sequence 54
7		22	1.4	22	6	I46567	I46567 Sequence 54
8		22	1.4	22	6	I46609	I46609 Sequence 58
9		22	1.4	22	6	I46716	I46716 Sequence 69
10		22	1.4	22	6	I46718	I46718 Sequence 69
11	c	21.8	1.4	25	6	AR434873	AR434873 Sequence
12		21	1.4	21	6	I46587	I46587 Sequence 56
13		21	1.4	21	6	I46598	I46598 Sequence 57
14		21	1.4	21	6	I46603	I46603 Sequence 58
15	c	20.8	1.3	25	6	AR434872	AR434872 Sequence
16	c	20.8	1.3	25	6	AR434874	AR434874 Sequence
17		20.4	1.3	22	6	I46549	I46549 Sequence 52
18		20.4	1.3	22	6	I46550	I46550 Sequence 52
19		20.4	1.3	22	6	I46554	I46554 Sequence 53
20		20.4	1.3	22	6	I46555	I46555 Sequence 53
21		20.4	1.3	22	6	I46557	I46557 Sequence 53
22		20.4	1.3	22	6	I46664	I46664 Sequence 64
23		20.4	1.3	22	6	I46723	I46723 Sequence 70
24		20.4	1.3	22	6	I46725	I46725 Sequence 70
25		20.4	1.3	22	6	I60472	I60472 Sequence 5
26	c	19.8	1.3	25	6	AR434871	AR434871 Sequence
27	c	19.8	1.3	25	6	AR434875	AR434875 Sequence
28		19.6	1.3	30	6	AR236072	AR236072 Sequence
29	c	19.6	1.3	30	6	AR236073	AR236073 Sequence
30		19.6	1.3	30	6	AX147143	AX147143 Sequence
31	c	19.6	1.3	30	6	AX147144	AX147144 Sequence
32	c	19.4	1.3	25	6	AR434869	AR434869 Sequence
33	c	19.4	1.3	25	6	AR434870	AR434870 Sequence
34		18.8	1.2	22	6	I46551	I46551 Sequence 53
35		18.8	1.2	22	6	I46666	I46666 Sequence 64
36		18.8	1.2	22	6	I46699	I46699 Sequence 67
37		18.8	1.2	22	6	I46700	I46700 Sequence 67
38		18.8	1.2	22	6	I46702	I46702 Sequence 68
39		18.8	1.2	22	6	I46703	I46703 Sequence 68
40		18.8	1.2	22	6	I46707	I46707 Sequence 68
41		18.8	1.2	22	6	I46710	I46710 Sequence 68
42		18.8	1.2	22	6	I46711	I46711 Sequence 69
43	c	18.8	1.2	25	6	AR434876	AR434876 Sequence
44		18.8	1.2	27	6	AX067196	AX067196 Sequence
45	c	18.8	1.2	27	6	AX067203	AX067203 Sequence

ALIGNMENTS

RESULT 1
I46576
LOCUS I46576 26 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 555 from patent US 5639612.
ACCESSION I46576
VERSION I46576.1 GI:2470541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Mitsuhashi,M. and Cooper,A.
TITLE Method for detecting polynucleotides with immobilized polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 555 17-JUN-1997;

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Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 2
I46581
LOCUS       I46581                  26 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 560 from patent US 5639612.
ACCESSION   I46581
VERSION     I46581.1  GI:2470546
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 560 17-JUN-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
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Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 3
I46686
LOCUS       I46686                  26 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 665 from patent US 5639612.
ACCESSION   I46686
VERSION     I46686.1  GI:2470651
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 665 17-JUN-1997;
FEATURES             Location/Qualifiers
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Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 4
I46693
LOCUS       I46693                  26 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 672 from patent US 5639612.
ACCESSION   I46693
VERSION     I46693.1  GI:2470658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 672 17-JUN-1997;
FEATURES             Location/Qualifiers
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Qy        921 TGCCAGTTTGAAGATCTGAACAGAAG 946
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Db          1 TGCCAGTTTGAAGATCTGAACCGAAG 26


RESULT 5
I46548
LOCUS       I46548                  22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 527 from patent US 5639612.
ACCESSION   I46548
VERSION     I46548.1  GI:2470513
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 527 17-JUN-1997;
FEATURES             Location/Qualifiers
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Qy        147 AGCACCATTGTGAAACAGATGA 168
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Db          1 AGCACCATTGTGAAACAGATGA 22


RESULT 6
I46562
LOCUS       I46562                  22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 541 from patent US 5639612.
ACCESSION   I46562
VERSION     I46562.1  GI:2470527
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
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  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 541 17-JUN-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        601 TGTTTGATGTAGGTGGCCAAAG 622
              ||||||||||||||||||||||
Db          1 TGTTTGATGTAGGTGGCCAAAG 22


RESULT 7
I46567
LOCUS       I46567                   22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 546 from patent US 5639612.
ACCESSION   I46567
VERSION     I46567.1  GI:2470532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 546 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .22
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ORIGIN

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Qy        601 TGTTTGATGTAGGTGGCCAAAG 622
              ||||||||||||||||||||||
Db          1 TGTTTGATGTAGGTGGCCAAAG 22


RESULT 8
I46609
LOCUS       I46609                   22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 588 from patent US 5639612.
ACCESSION   I46609
VERSION     I46609.1  GI:2470574
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 588 17-JUN-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        498 CAGTCTAACTACATTCCAACTC 519
              ||||||||||||||||||||||
Db          1 CAGTCTAACTACATTCCAACTC 22


RESULT 9
I46716
LOCUS       I46716                   22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 695 from patent US 5639612.
ACCESSION   I46716
VERSION     I46716.1  GI:2470681
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 695 17-JUN-1997;
FEATURES             Location/Qualifiers
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Qy        331 TTGTTTTAGCTGGCAGTGCTGA 352
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Db          1 TTGTTTTAGCTGGCAGTGCTGA 22


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I46718
LOCUS       I46718                   22 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 697 from patent US 5639612.
ACCESSION   I46718
VERSION     I46718.1  GI:2470683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
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  JOURNAL   Patent: US 5639612-A 697 17-JUN-1997;
FEATURES             Location/Qualifiers
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Qy        331 TTGTTTTAGCTGGCAGTGCTGA 352
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Db          1 TTGTTTTAGCTGGCAGTGCTGA 22


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LOCUS       AR434873                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1296 from patent US 6656700.
ACCESSION   AR434873
VERSION     AR434873.1  GI:40197716
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1296 02-DEC-2003;
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Db         25 CTTTCTTTTTTTTTCCCCCCTTCTT 1


RESULT 12
I46587
LOCUS       I46587                   21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 566 from patent US 5639612.
ACCESSION   I46587
VERSION     I46587.1  GI:2470552
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
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  JOURNAL   Patent: US 5639612-A 566 17-JUN-1997;
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Db          1 GACGGCTAAAGATTGACTTTG 21


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DEFINITION  Sequence 577 from patent US 5639612.
ACCESSION   I46598
VERSION     I46598.1  GI:2470563
KEYWORDS    .
SOURCE      Unknown.
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            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
            polynucleotide probes identified based on T.sub.m
  JOURNAL   Patent: US 5639612-A 577 17-JUN-1997;
FEATURES             Location/Qualifiers
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Db          1 TCTTCGGACGAGAGTGAAGAC 21


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DEFINITION  Sequence 582 from patent US 5639612.
ACCESSION   I46603
VERSION     I46603.1  GI:2470568
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SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 21)
  AUTHORS   Mitsuhashi,M. and Cooper,A.
  TITLE     Method for detecting polynucleotides with immobilized
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  JOURNAL   Patent: US 5639612-A 582 17-JUN-1997;
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DEFINITION  Sequence 1295 from patent US 6656700.
ACCESSION   AR434872
VERSION     AR434872.1  GI:40197715
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1295 02-DEC-2003;
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Db         25 TTTCTTTTTTTTTCCCCCCTTCTT 2


Search completed: September 14, 2004, 15:46:56
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 12:52:25 ; Search time 622 Seconds
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10538.536 Million cell updates/sec

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Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqn2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	26	1.7	26	2	AAQ47436	Aaq47436 Human G p
	2	26	1.7	26	2	AAQ47441	Aaq47441 Rat G pro
	3	26	1.7	26	2	AAQ47449	Aaq47449 Rat G pro
	4	24.4	1.6	26	2	AAQ47456	Aaq47456 Rat G pro
	5	24.2	1.6	29	9	ADB89210	Adb89210 Human Gia
	6	24.2	1.6	29	9	ADC24557	Adc24557 Human Gi
	7	24.2	1.6	29	9	ADD67827	Add67827 Human bet
	8	24.2	1.6	29	9	ADE10540	Ade10540 Minicell
	9	24.2	1.6	29	9	ADE11462	Ade11462 Human Gia
	10	24.2	1.6	29	9	ADE12640	Ade12640 Human Gia
	11	24.2	1.6	29	9	ADE12403	Ade12403 Human Gia
	12	23	1.5	23	3	AAA15503	Aaa15503 Human G-a
c	13	23	1.5	23	3	AAA15504	Aaa15504 Human G-a
	14	22	1.4	22	2	AAQ47412	Aaq47412 Human G p
	15	22	1.4	22	2	AAQ47429	Aaq47429 Rat G pro
	16	22	1.4	22	2	AAQ47504	Aaq47504 G protein
	17	22	1.4	22	2	AAQ47424	Aaq47424 Human G p
	18	22	1.4	22	2	AAQ47501	Aaq47501 Rat G pro
	19	22	1.4	22	2	AAQ47497	Aaq47497 G protein
	20	22	1.4	22	2	AAQ47508	Aaq47508 Rat G pro
	21	22	1.4	22	2	AAQ47514	Aaq47514 Human G p
	22	22	1.4	22	2	AAQ47397	Aaq47397 G protein
	23	22	1.4	22	3	AAA15505	Aaa15505 Human G-a
c	24	22	1.4	30	9	ADB89211	Adb89211 Human Gia
c	25	22	1.4	30	9	ADC24558	Adc24558 Human Gi
c	26	22	1.4	30	9	ADD67828	Add67828 Human bet
c	27	22	1.4	30	9	ADE10541	Ade10541 Minicell
c	28	22	1.4	30	9	ADE11463	Ade11463 Human Gia
c	29	22	1.4	30	9	ADE12641	Ade12641 Human Gia
c	30	22	1.4	30	9	ADE12404	Ade12404 Human Gia
c	31	21.8	1.4	25	6	ABS75770	Abs75770 Human PAP
	32	21	1.4	21	2	AAQ47485	Aaq47485 G protein
	33	21	1.4	21	2	AAQ47493	Aaq47493 Rat G pro
	34	21	1.4	21	2	AAQ47462	Aaq47462 Human G p
c	35	21	1.4	21	2	AAQ47405	Aaq47405 G protein
	36	21	1.4	21	2	AAQ47488	Aaq47488 Human G p
c	37	20.8	1.3	25	6	ABS75769	Abs75769 Human PAP
c	38	20.8	1.3	25	6	ABS75771	Abs75771 Human PAP
	39	20.4	1.3	22	2	AAQ47419	Aaq47419 Rat G pro
	40	20.4	1.3	22	2	AAQ47413	Aaq47413 Human G p
	41	20.4	1.3	22	2	AAQ47383	Aaq47383 Sense G p
	42	20.4	1.3	22	2	AAQ47414	Aaq47414 Human G p
c	43	20.4	1.3	22	2	AAQ47401	Aaq47401 Common G
	44	20.4	1.3	22	2	AAQ47475	Aaq47475 Rat G pro
	45	20.4	1.3	22	2	AAQ47516	Aaq47516 Rat G pro

ALIGNMENTS

RESULT 1
AAQ47436
ID AAQ47436 standard; cDNA to mRNA; 26 BP.
XX
AC AAQ47436;
XX
DT 25-MAR-2003 (revised)
DT 26-JAN-1994 (first entry)
XX
DE Human G protein, Gi-3, primer HUMGIAB 178.
XX
KW Probe; quantification; human; GTP binding protein; G protein;
KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW pathophysiology; disease state; hereditary; cancer; infectious;
KW osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
KW PCR; ss.
XX
OS Synthetic.
XX
PN WO9315221-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000977.
XX
PR 29-JAN-1992; 92US-00827208.
PR 24-MAR-1992; 92US-00857059.
PR 12-NOV-1992; 92US-00974409.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Akitaya T, Cooper A, Mitsuhashi M;
XX
DR WPI; 1993-258695/32.
XX
PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT having sequence complementary to sequence unique to the MRNA.
XX
PS Claim 15 and 38; Page 46; 177pp; English.
XX
CC The sequences given in AAQ47433-44 are primers which were used in the
CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These primers are derived from human and rat G-protein sequences. These
CC primers were used in conjunction with the method of the invention, in
CC PCR, for the detection and quantification of mRNAs in a sample without

CC the need to purify the mRNA from cells. The claimed method comprises
CC identifying a polynucleotide sequence unique to the mRNA, and
CC immobilising an oligomer complementary to this sequence to an insoluble
CC support. The sample is then incubated with the insoluble support such
CC that the unique sequence will hybridise to the bound oligomer and be
CC immobilised. Non-immobilised components are washed from the support and
CC bound RNA is labelled in such a way that the label is incorporated onto
CC the support relative to the amount of mRNA on the support. The amount of
CC bound label is then determined. This method can be used for the reliable,
CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
CC be used for diagnosing and recognition of pathophysiology of various
CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
CC G proteins are thought to be involved in causing various disease states.
CC A genetic deficiency of Gs protein is the molecular basis of hereditary
CC osteodystrophy. Pituitary tumours in acromegalic patients have been shown
CC to contain mutant Gs proteins. G proteins are also involved in invasive
CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGGACGAGAGTGAAGAC 550
||||||||||||||||||||||||||
Db 1 GATGTTCTTCGGACGAGAGTGAAGAC 26

RESULT 2
AAQ47441
ID AAQ47441 standard; cDNA to mRNA; 26 BP.
XX
AC AAQ47441;
XX
DT 25-MAR-2003 (revised)
DT 26-JAN-1994 (first entry)
XX
DE Rat G protein, Gi-3, primer RATBPGTP 183.
XX
KW Probe; quantification; human; GTP binding protein; G protein;
KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW pathophysiology; disease state; hereditary; cancer; infectious;
KW osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
KW PCR; ss.
XX
OS Synthetic.
XX
PN WO9315221-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000977.
XX
PR 29-JAN-1992; 92US-00827208.
PR 24-MAR-1992; 92US-00857059.
PR 12-NOV-1992; 92US-00974409.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Akitaya T, Cooper A, Mitsuhashi M;
XX
DR WPI; 1993-258695/32.
XX
PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT having sequence complementary to sequence unique to the MRNA.
XX
PS Claim 15 and 38; Page 46; 177pp; English.
XX
CC The sequences given in AAQ47433-44 are primers which were used in the
CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These primers are derived from human and rat G-protein sequences. These
CC primers were used in conjunction with the method of the invention, in
CC PCR, for the detection and quantification of mRNAs in a sample without
CC the need to purify the mRNA from cells. The claimed method comprises
CC identifying a polynucleotide sequence unique to the mRNA, and
CC immobilising an oligomer complementary to this sequence to an insoluble
CC support. The sample is then incubated with the insoluble support such
CC that the unique sequence will hybridise to the bound oligomer and be
CC immobilised. Non-immobilised components are washed from the support and
CC bound RNA is labelled in such a way that the label is incorporated onto
CC the support relative to the amount of mRNA on the support. The amount of
CC bound label is then determined. This method can be used for the reliable,
CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
CC be used for diagnosing and recognition of pathophysiology of various
CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
CC G proteins are thought to be involved in causing various disease states.
CC A genetic deficiency of Gs protein is the molecular basis of hereditary
CC osteodystrophy. Pituitary tumours in acromegalic patients have been shown
CC to contain mutant Gs proteins. G proteins are also involved in invasive
CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGGACGAGAGTGAAGAC 550
||||||||||||||||||||||||||
Db 1 GATGTTCTTCGGACGAGAGTGAAGAC 26

RESULT 3
AAQ47449
ID AAQ47449 standard; cDNA to mRNA; 26 BP.
XX
AC AAQ47449;
XX
DT 25-MAR-2003 (revised)
DT 26-JAN-1994 (first entry)
XX
DE Rat G protein, Gi-3, probe RATBPGTP 230.
XX
KW Probe; quantification; human; GTP binding protein; G protein;
KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW pathophysiology; disease state; hereditary; cancer; infectious;
KW osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
KW PCR; ss.
XX
OS Synthetic.
XX
PN WO9315221-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000977.
XX
PR 29-JAN-1992; 92US-00827208.
PR 24-MAR-1992; 92US-00857059.
PR 12-NOV-1992; 92US-00974409.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Akitaya T, Cooper A, Mitsuhashi M;
XX
DR WPI; 1993-258695/32.
XX
PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT having sequence complementary to sequence unique to the MRNA.
XX
PS Claim 14 and 38; Page 47; 177pp; English.

XX
CC The sequences given in AAQ47445-51 are probes which were used in the
CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These probes are derived from human and rat G-protein sequences. These
CC probes were used in the method of the invention, for the detection and
CC quantification of mRNAs in a sample without the need to purify the mRNA
CC from cells. The claimed method comprises identifying a polynucleotide
CC sequence unique to the mRNA, and immobilising an oligomer complementary
CC to this sequence to an insoluble support. The sample is then incubated
CC with the insoluble support such that the unique sequence will hybridise
CC to the bound oligomer and be immobilised. Non-immobilised components are
CC washed from the support and bound RNA is labelled in such a way that the
CC label is incorporated onto the support relative to the amount of mRNA on
CC the support. The amount of bound label is then determined. This method
CC can be used for the reliable, rapid, simultaneous quantification of
CC multiple varieties of mRNA. It may be used for diagnosing and recognition
CC of pathophysiology of various disease states, eg. hereditary diseases,
CC cancer, and infectious diseases. G proteins are thought to be involved in
CC causing various disease states. A genetic deficiency of Gs protein is the
CC molecular basis of hereditary osteodystrophy. Pituitary tumours in
CC acromegalic patients have been shown to contain mutant Gs proteins. G
CC proteins are also involved in invasive and metastatic melanoma cells, and
CC diabetes. See also AAQ47381-666. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGGACGAGAGTGAAGAC 550
||||||||||||||||||||||||||
Db 1 GATGTTCTTCGGACGAGAGTGAAGAC 26

RESULT 4
AAQ47456
ID AAQ47456 standard; cDNA to mRNA; 26 BP.
XX
AC AAQ47456;
XX
DT 25-MAR-2003 (revised)
DT 26-JAN-1994 (first entry)
XX
DE Rat G protein, Gi-3, probe RATBPGTP 231.
XX
KW Probe; quantification; human; GTP binding protein; G protein;
KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW pathophysiology; disease state; hereditary; cancer; infectious;
KW osteodystrophy; pituitary tumour; acromegaly; melanomer cells; diabetes;
KW PCR; ss.
XX
OS Synthetic.
XX
PN WO9315221-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000977.
XX
PR 29-JAN-1992; 92US-00827208.
PR 24-MAR-1992; 92US-00857059.
PR 12-NOV-1992; 92US-00974409.
XX
PA (HITB) HITACHI CHEM CO LTD.
PA (HITB) HITACHI CHEM RES CENT INC.
XX
PI Akitaya T, Cooper A, Mitsuhashi M;
XX
DR WPI; 1993-258695/32.
XX
PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT having sequence complementary to sequence unique to the MRNA.
XX
PS Claim 14 and 38; Page 47; 177pp; English.
XX
CC The sequences given in AAQ47452-58 are probes which were used in the
CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These probes are derived from human and rat G-protein sequences. These
CC probes were used in the method of the invention, for the detection and
CC quantification of mRNAs in a sample without the need to purify the mRNA
CC from cells. The claimed method comprises identifying a polynucleotide
CC sequence unique to the mRNA, and immobilising an oligomer complementary
CC to this sequence to an insoluble support. The sample is then incubated
CC with the insoluble support such that the unique sequence will hybridise
CC to the bound oligomer and be immobilised. Non-immobilised components are
CC washed from the support and bound RNA is labelled in such a way that the
CC label is incorporated onto the support relative to the amount of mRNA on
CC the support. The amount of bound label is then determined. This method
CC can be used for the reliable, rapid, simultaneous quantification of
CC multiple varieties of mRNA. It may be used for diagnosing and recognition
CC of pathophysiology of various disease states, eg. hereditary diseases,
CC cancer, and infectious diseases. G proteins are thought to be involved in
CC causing various disease states. A genetic deficiency of Gs protein is the
CC molecular basis of hereditary osteodystrophy. Pituitary tumours in
CC acromegalic patients have been shown to contain mutant Gs proteins. G
CC proteins are also involved in invasive and metastatic melanomer cells,
CC and diabetes. See also AAQ47381-666. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 26 BP; 8 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.4; DB 2; Length 26;
Best Local Similarity 96.2%; Pred. No. 1.6e+04;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 921 TGCCAGTTTGAAGATCTGAACAGAAG 946
|||||||||||||||||||| ||||
Db 1 TGCCAGTTTGAAGATCTGAACCGAAG 26

RESULT 5
ADB89210
ID ADB89210 standard; DNA; 29 BP.
XX
AC ADB89210;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human Gialpha construct PCR primer #1.
XX
KW ss; cytostatic; gene therapy; minicell; membrane protein; cancer; human;
KW PCR; primer.
XX
OS Homo sapiens.
XX
PN US2003166099-A1.
XX
PD 04-SEP-2003.
XX
PF 28-MAY-2002; 2002US-00157305.
XX
PR 05-JUN-2001; 2001US-0295566P.
PR 25-FEB-2002; 2002US-0359843P.
XX
PA (SABB/) SABBADINI R A.
PA (SURB/) SURBER M W.
PA (BERK/) BERKLEY N.
PA (SEGA/) SEGALL A M.
PA (KLEP/) KLEPPER R.
XX
PI Sabbadini RA, Surber MW, Berkley N, Segall AM, Klepper R;
XX
DR WPI; 2003-711671/67.
XX

PT New minicell comprising a membrane protein consisting of eukaryotic,
PT archeabacterial protein or organellar protein, useful for preparing a
PT composition for treating or preventing e.g. cancer.
XX
PS Example 22; Page 142; 0pp; English.
XX
CC The invention relates to a new minicell comprising a membrane protein
CC comprising eukaryotic membrane protein, archeabacterial membrane protein
CC or organellar membrane protein. The minicell comprises membrane
CC conjugate, membrane fusion protein, eubacterial minicell, poroplast,
CC spheroplast, protoplast, biologically active compound or expression
CC construct, where the first expression construct comprises expression
CC sequences operably linked to an ORF (open reading frame) that encodes a
CC membrane protein. It comprises a second expression construct, having
CC sequences operably linked to a gene. The expression sequences are
CC inducible and/or repressible. The membrane conjugate comprises a membrane
CC protein chemically linked to a conjugated compound. The conjugated
CC compound comprises nucleic acid, polypeptide, lipid or small molecule.
CC The gene product of the gene is a nucleic acid or polypeptide and
CC regulates the expression of the ORF that encodes the protein. The
CC polypeptide is a membrane protein, soluble protein or secreted protein.
CC The membrane protein is a membrane fusion protein comprising a first
CC polypeptide, comprising at least one transmembrane domain or at least one
CC transmembrane anchoring domain, and a second polypeptide. The second
CC polypeptide is not derived from a eubacterial protein and is neither a
CC His tag nor a glutathione-S-transferase polypeptide. The minicell is
CC useful for preparing a composition for treating or preventing cancer. The
CC present sequence is PCR primer used in the construction of a DNA
CC expression construct used to test the minicell of the invention,
CC comprising a human gene (or fragment).
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 6
ADC24557
ID ADC24557 standard; DNA; 29 BP.
XX
AC ADC24557;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human Gi alpha cDNA PCR primer #1.
XX
KW ss; minicell; episomal expression construct; cancer; asthma; allergy;
KW inflammation; rheumatoid arthritis; diabetes; Alzheimer's disease;
KW Parkinson's disease; HIV; bacterial infection; hepatitis;
KW myocardial ischaemia; human; PCR; primer.
XX
OS Homo sapiens.
XX
PN US2003190749-A1.
XX
PD 09-OCT-2003.
XX
PF 28-MAY-2002; 2002US-00157215.
XX
PR 24-MAY-2001; 2001US-0293566P.
PR 25-FEB-2002; 2002US-0359843P.
PR 24-MAY-2002; 2002US-00154951.
XX
PA (SURB/) SURBER M W.
PA (SABB/) SABBADINI R A.
PA (SEGA/) SEGALL A M.
PA (BERK/) BERKLEY N.
XX
PI Surber MW, Sabbadini RA, Segall AM, Berkley N;
XX
DR WPI; 2003-831632/77.
XX
PT New minicell-producing parent cell comprising an expression element and a
PT mutation in an endogenous gene, useful for producing achromosomal and
PT anucleate cells for diagnostic or therapeutic purposes and for drug
PT discovery.
XX
PS Example 22; SEQ ID NO 204; 242pp; English.
XX
CC The invention relates to a minicell-producing parent cell. The parent
CC cell comprises: an expression element that comprises a gene operably
CC linked to expression sequences that are inducible and/or repressible,
CC where induction or repression of the gene regulates the copy number of an
CC episomal expression construct and/or causes or enhances the production of
CC minicells; and/or a mutation in an endogenous gene, where the mutation
CC regulates the copy number of an episomal expression construct and/or
CC causes or enhances minicell production. Also disclosed are compositions
CC and methods for preparing the minicells (or a soluble and/or secreted
CC protein, or antibodies and/or antibody derivatives that recognise an
CC immunogenic epitope on the native form of a membrane protein, a method of
CC associating a radioactive compound with a cell), a method of transferring
CC a membrane protein from a minicell membrane to a biological membrane, a
CC pharmaceutical composition comprising the minicell, a method of making
CC the above pharmaceutical composition, a method of detecting an agent that
CC is specifically bound by a binding moiety, a method of in situ imaging of
CC a tissue or organ, methods of determining the rate or amount of transfer
CC of nucleic acid from a minicell to a cell, a method of determining the
CC three-dimensional structure of a membrane protein, a method of
CC identifying ligand-interacting atoms in a defined three-dimensional
CC structure of a target protein, methods of identifying a nucleic acid that
CC encodes the above protein, and methods of bioremediation. The minicell-
CC producing parent cell is useful for producing achromosomal and anucleate
CC cells for diagnostic and therapeutic applications (e.g. in diagnosing or
CC treating cancer, asthma, allergies, inflammation, rheumatoid arthritis,
CC diabetes, Alzheimer's disease, Parkinson's disease, HIV, bacterial
CC infections, hepatitis or myocardial ischaemia), as well as research tools
CC and agents for drug discovery or for delivery of nucleic acids and other
CC bioactive compounds to cells. The present sequence is a human PCR primer
CC used to construct a recombinant DNA for inclusion in a mini-cell of the
CC invention. Note: The authors have mixed up the seq id numbers between the
CC disclosure and the sequence listing. This means that several of the
CC sequences cannot be conclusively identified and some of the rest may be
CC mis-identified.
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 7
ADD67827
ID ADD67827 standard; DNA; 29 BP.
XX
AC ADD67827;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human beta-2 adrenergic receptor/ToxR construct.
XX
KW Minicell; ds; membrane protein; transmembrane domain;
KW membrane anchoring domain; Type III secretion system; achromosomal cell;
KW anucleate cell; cancer; asthma; allergy; inflammation;
KW rheumatoid arthritis; diabetes; Alzheimer's disease; Parkinson's disease;
KW HIV infection; bacterial infection; hepatitis; myocardial ischaemia;

KW human.
XX
OS Synthetic.
OS Homo sapiens.
OS Vibrio cholerae.
XX
PN US2003194714-A1.
XX
PD 16-OCT-2003.
XX
PF 28-MAY-2002; 2002US-00157299.
XX
PR 05-JUN-2001; 2001US-0295566P.
PR 25-FEB-2002; 2002US-0359843P.
XX
PA (SABB/) SABBADINI R A.
PA (BERK/) BERKLEY N.
PA (SURB/) SURBER M W.
XX
PI Sabbadini RA, Berkley N, Surber MW;
XX
DR WPI; 2003-844449/78.
XX
PT New minicell useful for producing achromosomal and anucleate cells for
PT diagnosing or treating e.g. cancer, asthma, allergies, inflammation,
PT diabetes, Alzheimer's disease or HIV, and as research tools and agents
PT for drug discovery.
XX
PS Example 22; SEQ ID NO 204; 244pp; English.
XX
CC The invention relates to a minicell comprising at least one nucleic acid.
CC The minicell displays a binding moiety directed to a target compound,
CC where the binding moiety is selected from a eukaryotic membrane protein,
CC an archeabacterial membrane protein, an organellar membrane protein, and
CC a fusion protein. The fusion protein comprises a first polypeptide
CC comprising at least one transmembrane domain or at least one membrane
CC anchoring domain, and a second polypeptide that is not derived from a
CC eubacterial protein and is neither a His tag nor a glutathione-S-
CC transferase polypeptide, where the polypeptide comprises a binding
CC moiety. Also included is the method of introducing a nucleic acid into a
CC cell, comprising contacting the cell with the minicell cited above. The
CC minicell is selected from a eubacterial minicell, a poroplast, a
CC spheroplast and a protoplast. The nucleic acid comprises an expression
CC construct comprising expression sequences operably linked to an ORF
CC encoding the proteins mentioned above or encoding a therapeutic
CC polypeptide. The therapeutic polypeptide is a membrane polypeptide or a
CC soluble polypeptide. The soluble polypeptide comprises a cellular
CC secretion sequence. The expression sequences are inducible and/or
CC repressible. These are induced and/or depressed when the binding moiety
CC displayed by the minicell binds to its target compound. The ORF encodes a
CC polypeptide having an amino acid sequence that facilitates cellular
CC transfer of a biologically active compound contained within or displayed
CC by the minicell. The membrane of the minicell comprises a system for
CC transferring a molecule from the interior of a minicell into the
CC cytoplasm of the cell. The system is a Type III secretion system. The
CC minicell and method are useful in producing achromosomal and anucleate
CC cells for diagnostic and therapeutic applications (e.g. in diagnosing or
CC treating cancer, asthma, allergies, inflammation, rheumatoid arthritis,
CC diabetes, Alzheimer's disease, Parkinson's disease, HIV, bacterial
CC infections, hepatitis or myocardial ischaemia), as well as research tools
CC and agents for drug discovery or for delivery of nucleic acids and other
CC bioactive compounds to cells. The present sequence is a minicell
CC construct incorporating human DNA sequence from a gene of interest.
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 8
ADE10540
ID ADE10540 standard; DNA; 29 BP.
XX
AC ADE10540;
XX
DT 29-JAN-2004 (first entry)
XX
DE Minicell associated DNA expression construct PCR primer #73.
XX
KW membrane protein transfer; minicell membrane; biological membrane;
KW hyperproliferative disorder; cancer; ss; PCR; primer.
XX
OS Synthetic.
XX
PN US2003199089-A1.
XX
PD 23-OCT-2003.
XX
PF 28-MAY-2002; 2002US-00157318.
XX
PR 05-JUN-2001; 2001US-0295566P.
PR 25-FEB-2002; 2002US-0359843P.
XX
PA (SURB/) SURBER M W.
PA (SABB/) SABBADINI R A.
XX
PI Surber MW, Sabbadini RA;
XX
DR WPI; 2003-852795/79.
XX
PT Transferring a membrane protein from a minicell membrane to a biological
PT membrane for diagnosing or treating e.g. cancer by allowing the minicell
PT and biological membrane to remain in contact for a sufficient time for
PT the transfer to occur.
XX
PS Example 22; SEQ ID NO 204; 243pp; English.
XX
CC The invention relates to a method of transferring a membrane protein from
CC a minicell membrane to a biological membrane which comprises contacting a
CC minicell to the biological membrane and allowing the minicell and
CC biological membrane to remain in contact for a period of time sufficient
CC for the transfer to occur. The method is useful for transferring a
CC membrane protein from a minicell membrane to a biological membrane for
CC preparing a composition for diagnosing or treating hyperproliferative
CC disorders, e.g. cancer. The present sequence represents a minicell
CC associated DNA expression construct PCR primer.
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 9
ADE11462
ID ADE11462 standard; DNA; 29 BP.
XX
AC ADE11462;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Galpha XhoI-ClaI fragment PCR primer #1.
XX
KW Minicell; eukaryotic expression sequence; open reading frame; ORF;
KW eubacterial minicell; poroplast; spheroplast; protoplast;

KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
KW primer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003166279-A1.
XX
PD 04-SEP-2003.
XX
PF 28-MAY-2002; 2002US-00157391.
XX
PR 24-MAY-2001; 2001US-0293566P.
PR 25-FEB-2002; 2002US-0359843P.
PR 24-MAY-2002; 2002US-00154951.
XX
PA (SABB/) SABBADINI R A.
PA (BERK/) BERKLEY N.
XX
PI Sabbadini RA, Berkley N;
XX
DR WPI; 2003-874920/81.
XX
PT Determining the rate of transfer of nucleic acid from a minicell to a
PT cell (and vice versa) useful in the production of achromosomal and
PT anucleate cells used for diagnostic and therapeutic applications.
XX
PS Example 22; SEQ ID NO 204; 242pp; English.
XX
CC The invention relates to determining the rate of transfer of nucleic acid
CC from a minicell to a cell, determining the amount of a nucleic acid
CC transferred to a cell from a minicell and detecting the expression of an
CC expression element in a cell. The minicell comprises an expression
CC element having eukaryotic expression sequences operably linked to an open
CC reading frame (ORF) encoding a detectable polypeptide, the minicells
CC display a binding group and the binding group displays an epitope of the
CC cell. The minicell is a eubacterial minicell, a poroplast, a spheroplast
CC or a protoplast. The cell is a eukaryotic cell. The binding group is an
CC antibody or antibody derivative, especially a single-chain antibody, an
CC aptamer or an organic compound. The detectable polypeptide is a
CC fluorescent polypeptide. The methods are used in the production of
CC achromosomal and anucleate cells useful for applications such as
CC diagnostic and therapeutic uses, as well as research tools and agents for
CC drug discovery. The present sequence is a PCR primer used to construct a
CC minicell construct of the invention incorporating a human DNA sequence.
CC Note: The authors have mixed up the SEQ ID numbers between the text and
CC the sequence listing such that some of the sequences cannot be
CC conclusively identified.
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 10
ADE12640
ID ADE12640 standard; DNA; 29 BP.
XX
AC ADE12640;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Gialpha XhoI-ClaI fragment PCR primer #1.
XX
KW Minicell; eukaryotic expression sequence; open reading frame; ORF;
KW eubacterial minicell; poroplast; spheroplast; protoplast;
KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
KW primer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003190601-A1.
XX
PD 09-OCT-2003.
XX
PF 28-MAY-2002; 2002US-00157096.
XX
PR 24-MAY-2001; 2001US-0293566P.
PR 25-FEB-2002; 2002US-0359843P.
PR 24-MAY-2002; 2002US-00154951.
XX
PA (SABB/) SABBADINI R A.
PA (BERK/) BERKLEY N.
PA (SURB/) SURBER M W.
XX
PI Sabbadini RA, Berkley N, Surber MW;
XX
DR WPI; 2003-875310/81.
XX
PT Identifying an agent that specifically binds a target compound,
PT especially a membrane protein, comprises contacting a minicell displaying
PT the target compound with a library of compounds.
XX
PS Example 22; SEQ ID NO 204; 242pp; English.
XX
CC The invention relates to determining the rate of transfer of nucleic acid
CC from a minicell to a cell, determining the amount of a nucleic acid
CC transferred to a cell from a minicell and detecting the expression of an
CC expression element in a cell. The minicell comprises an expression
CC element having eukaryotic expression sequences operably linked to an open
CC reading frame (ORF) encoding a detectable polypeptide, the minicells
CC display a binding group and the binding group displays an epitope of the
CC cell. The minicell is a eubacterial minicell, a poroplast, a spheroplast
CC or a protoplast. The cell is a eukaryotic cell. The binding group is an
CC antibody or antibody derivative, especially a single-chain antibody, an
CC aptamer or an organic compound. The detectable polypeptide is a
CC fluorescent polypeptide. The methods are used in the production of
CC achromosomal and anucleate cells useful for applications such as
CC diagnostic and therapeutic uses, as well as research tools and agents for
CC drug discovery. The present sequence is a PCR primer used to construct a
CC minicell construct of the invention incorporating a human DNA sequence.
CC Note: The authors have mixed up the SEQ ID numbers between the text and
CC the sequence listing such that some of the sequences cannot be
CC conclusively identified.
XX
SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
||||||||| |||||||||| |||||||
Db 1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29

RESULT 11
ADE12403
ID ADE12403 standard; DNA; 29 BP.
XX
AC ADE12403;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Gialpha XhoI-ClaI fragment PCR primer #1.
XX
KW Minicell; eukaryotic expression sequence; open reading frame; ORF;
KW eubacterial minicell; poroplast; spheroplast; protoplast;
KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;

```
KW   primer.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003207833-A1.
XX
PD   06-NOV-2003.
XX
PF   28-MAY-2002; 2002US-00156811.
XX
PR   25-FEB-2002; 2002US-0359843P.
XX
PA   (BERK/) BERKLEY N.
PA   (KLEP/) KLEPPER R.
PA   (SABB/) SABBADINI R A.
XX
PI   Berkley N,  Klepper R,  Sabbadini RA;
XX
DR   WPI; 2003-875896/81.
XX
PT   Pharmaceutical composition comprising minicells, useful for preventing,
PT   treating or diagnosing cancer, asthma or HIV, or as reagents in drug
PT   discovery and functional proteomics, as research tools or in compound
PT   screening.
XX
PS   Example 22; SEQ ID NO 204; 243pp; English.
XX
CC   The invention relates to determining the rate of transfer of nucleic acid
CC   from a minicell to a cell, determining the amount of a nucleic acid
CC   transferred to a cell from a minicell and detecting the expression of an
CC   expression element in a cell. The minicell comprises an expression
CC   element having eukaryotic expression sequences operably linked to an open
CC   reading frame (ORF) encoding a detectable polypeptide, the minicells
CC   display a binding group and the binding group displays an epitope of the
CC   cell. The minicell is a eubacterial minicell, a poroplast, a spheroplast
CC   or a protoplast. The cell is a eukaryotic cell. The binding group is an
CC   antibody or antibody derivative, especially a single-chain antibody, an
CC   aptamer or an organic compound. The detectable polypeptide is a
CC   fluorescent polypeptide. The methods are used in the production of
CC   achromosomal and anucleate cells useful for applications such as
CC   diagnostic and therapeutic uses, as well as research tools and agents for
CC   drug discovery. The present sequence is a PCR primer used to construct a
CC   minicell construct of the invention incorporating a human DNA sequence.
CC   Note: The authors have mixed up the SEQ ID numbers between the text and
CC   the sequence listing such that some of the sequences cannot be
CC   conclusively identified.
XX
SQ   Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

  Query Match             1.6%;  Score 24.2;  DB 9;  Length 29;
  Best Local Similarity   89.7%;  Pred. No. 1.9e+04;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              |||||||||  |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29


RESULT 12
AAA15503
ID   AAA15503 standard; DNA; 23 BP.
XX
AC   AAA15503;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human G-alpha-i3 gene PCR forward primer.
XX
KW   Human; G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine;
KW   thyrotropin-releasing hormone; somatostatin; signal transduction pathway;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6063626-A.
XX
PD   16-MAY-2000.
XX
PF   24-JUN-1999;   99US-00339775.
XX
PR   24-JUN-1999;   99US-00339775.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-375497/32.
XX
PT   New antisense compounds targeting nucleic acids encoding human G-alpha-I3
PT   useful for treating diseases associated with G-alpha-I3 expression and as
PT   prophylaxis to prevent or delay infection, inflammation or tumor
PT   formation.
XX
PS   Example 13; Col 38; 30pp; English.
XX
CC   The present sequence is a PCR primer for the human G-alpha-i3 gene. The
CC   protein produced from this gene is a member of the G protein family, and
CC   more specifically of the Gi family. The Gi proteins are involved in
CC   hormonal inhibition of adenylyl cyclase and the regulation of plasma
CC   membrane enzymes. In addition, G-alpha-i3 has been shown to have a role
CC   in the dopamine, thyrotropin-releasing hormone and somatostatin signal
CC   transduction pathways. The specification describes a number of antisense
CC   oligonucleotides which modulate the expression of G-alpha-i3 and can be
CC   used to prevent infection, inflammation and tumours
XX
SQ   Sequence 23 BP; 6 A; 3 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             1.5%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        273 GGACGGCTAAAGATTGACTTTGG 295
              |||||||||||||||||||||||
Db          1 GGACGGCTAAAGATTGACTTTGG 23


RESULT 13
AAA15504/c
ID   AAA15504 standard; DNA; 23 BP.
XX
AC   AAA15504;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human G-alpha-i3 gene PCR reverse primer.
XX
KW   Human; G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine;
KW   thyrotropin-releasing hormone; somatostatin; signal transduction pathway;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6063626-A.
XX
PD   16-MAY-2000.
XX
PF   24-JUN-1999;   99US-00339775.
XX
PR   24-JUN-1999;   99US-00339775.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM;
XX
DR   WPI; 2000-375497/32.
```

```
XX
PT   New antisense compounds targeting nucleic acids encoding human G-alpha-I3
PT   useful for treating diseases associated with G-alpha-I3 expression and as
PT   prophylaxis to prevent or delay infection, inflammation or tumor
PT   formation.
XX
PS   Example 13; Col 38; 30pp; English.
XX
CC   The present sequence is a PCR primer for the human G-alpha-i3 gene. The
CC   protein produced from this gene is a member of the G protein family, and
CC   more specifically of the Gi family. The Gi proteins are involved in
CC   hormonal inhibition of adenylyl cyclase and the regulation of plasma
CC   membrane enzymes. In addition, G-alpha-i3 has been shown to have a role
CC   in the dopamine, thyrotropin-releasing hormone and somatostatin signal
CC   transduction pathways. The specification describes a number of antisense
CC   oligonucleotides which modulate the expression of G-alpha-i3 and can be
CC   used to prevent infection, inflammation and tumours
XX
SQ   Sequence 23 BP; 10 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             1.5%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+04;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        329 ATTTGTTTTAGCTGGCAGTGCTG 351
              |||||||||||||||||||||||
Db         23 ATTTGTTTTAGCTGGCAGTGCTG 1


RESULT 14
AAQ47412
ID   AAQ47412 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ47412;
XX
DT   25-MAR-2003  (revised)
DT   26-JAN-1994  (first entry)
XX
DE   Human G protein, Gi-3, primer HUMGIAB.
XX
KW   Probe; quantification; human; GTP binding protein; G protein;
KW   alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW   pathophysiology; disease state; hereditary; cancer; infectious;
KW   osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
KW   PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9315221-A1.
XX
PD   05-AUG-1993.
XX
PF   29-JAN-1993;   93WO-US000977.
XX
PR   29-JAN-1992;   92US-00827208.
PR   24-MAR-1992;   92US-00857059.
PR   12-NOV-1992;   92US-00974409.
XX
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (HITB ) HITACHI CHEM RES CENT INC.
XX
PI   Akitaya T,  Cooper A,  Mitsuhashi M;
XX
DR   WPI; 1993-258695/32.
XX
PT   Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT   having sequence complementary to sequence unique to the MRNA.
XX
PS   Claim 15 and 38; Page 44; 177pp; English.
XX
CC   The sequences given in AAQ47409-20 are primers which were used in the
CC   quantification of human GTP binding protein (G protein)-specific mRNAs.
CC   These primers were used in conjunction with the method of the invention,
CC   in PCR, for the detection and quantification of mRNAs in a sample without
CC   the need to purify the mRNA from cells. The claimed method comprises
CC   identifying a polynucleotide sequence unique to the mRNA, and
CC   immobilising an oligomer complementary to this sequence to an insoluble
CC   support. The sample is then incubated with the insoluble support such
CC   that the unique sequence will hybridise to the bound oligomer and be
CC   immobilised. Non-immobilised components are washed from the support and
CC   bound RNA is labelled in such a way that the label is incorporated onto
CC   the support relative to the amount of mRNA on the support. The amount of
CC   bound label is then determined. This method can be used for the reliable,
CC   rapid, simultaneous quantification of multiple varieties of mRNA. It may
CC   be used for diagnosing and recognition of pathophysiology of various
CC   disease states, eg. hereditary diseases, cancer, and infectious diseases.
CC   G proteins are thought to be involved in causing various disease states.
CC   A genetic deficiency of Gs protein is the molecular basis of hereditary
CC   osteodystrophy. Pituitary tumours in acromegalic patients have been shown
CC   to contain mutant Gs proteins. G proteins are also involved in invasive
CC   and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 22 BP; 9 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             1.4%;  Score 22;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+04;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 AGCACCATTGTGAAACAGATGA 168
              ||||||||||||||||||||||
Db          1 AGCACCATTGTGAAACAGATGA 22


RESULT 15
AAQ47429
ID   AAQ47429 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ47429;
XX
DT   25-MAR-2003  (revised)
DT   26-JAN-1994  (first entry)
XX
DE   Rat G protein, Gi-3, primer RATBPGTP 169.
XX
KW   Probe; quantification; human; GTP binding protein; G protein;
KW   alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
KW   pathophysiology; disease state; hereditary; cancer; infectious;
KW   osteodystrophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
KW   PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9315221-A1.
XX
PD   05-AUG-1993.
XX
PF   29-JAN-1993;   93WO-US000977.
XX
PR   29-JAN-1992;   92US-00827208.
PR   24-MAR-1992;   92US-00857059.
PR   12-NOV-1992;   92US-00974409.
XX
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (HITB ) HITACHI CHEM RES CENT INC.
XX
PI   Akitaya T,  Cooper A,  Mitsuhashi M;
XX
DR   WPI; 1993-258695/32.
XX
PT   Quantitating messenger RNA in sample - using immobilised-polynucleotide
PT   having sequence complementary to sequence unique to the MRNA.
XX
PS   Claim 15 and 38; Page 45; 177pp; English.
XX
CC   The sequences given in AAQ47421-32 are primers which were used in the
```

CC quantification of human GTP binding protein (G protein)-specific mRNAs.
CC These primers were used in conjunction with the method of the invention,
CC in PCR, for the detection and quantification of mRNAs in a sample without
CC the need to purify the mRNA from cells. The claimed method comprises
CC identifying a polynucleotide sequence unique to the mRNA, and
CC immobilising an oligomer complementary to this sequence to an insoluble
CC support. The sample is then incubated with the insoluble support such
CC that the unique sequence will hybridise to the bound oligomer and be
CC immobilised. Non-immobilised components are washed from the support and
CC bound RNA is labelled in such a way that the label is incorporated onto
CC the support relative to the amount of mRNA on the support. The amount of
CC bound label is then determined. This method can be used for the reliable,
CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
CC be used for diagnosing and recognition of pathophysiology of various
CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
CC G proteins are thought to be involved in causing various disease states.
CC A genetic deficiency of Gs protein is the molecular basis of hereditary
CC osteodystrophy. Pituitary tumours in acromegalic patients have been shown
CC to contain mutant Gs proteins. G proteins are also involved in invasive
CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 22 BP; 5 A; 2 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 1.4%; Score 22; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        601 TGTTTGATGTAGGTGGCCAAAG 622
              ||||||||||||||||||||||
Db          1 TGTTTGATGTAGGTGGCCAAAG 22
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 628400

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	26	1.7	26	1	US-08-379-078-555	Sequence 555, App
	2	26	1.7	26	1	US-08-379-078-560	Sequence 560, App
	3	26	1.7	26	1	US-08-379-078-665	Sequence 665, App
	4	26	1.7	26	4	US-07-974-409C-178	Sequence 178, App
	5	26	1.7	26	4	US-07-974-409C-183	Sequence 183, App
	6	26	1.7	26	4	US-07-974-409C-230	Sequence 230, App
	7	26	1.7	26	5	PCT-US93-00977-178	Sequence 178, App
	8	26	1.7	26	5	PCT-US93-00977-183	Sequence 183, App
	9	26	1.7	26	5	PCT-US93-00977-230	Sequence 230, App
	10	24.4	1.6	26	1	US-08-379-078-672	Sequence 672, App
	11	24.4	1.6	26	4	US-07-974-409C-231	Sequence 231, App
	12	24.4	1.6	26	5	PCT-US93-00977-231	Sequence 231, App
	13	23	1.5	23	3	US-09-339-775-2	Sequence 2, Appli
c	14	23	1.5	23	3	US-09-339-775-3	Sequence 3, Appli
	15	22	1.4	22	1	US-08-379-078-527	Sequence 527, App
	16	22	1.4	22	1	US-08-379-078-541	Sequence 541, App
	17	22	1.4	22	1	US-08-379-078-546	Sequence 546, App
	18	22	1.4	22	1	US-08-379-078-588	Sequence 588, App
	19	22	1.4	22	1	US-08-379-078-695	Sequence 695, App
	20	22	1.4	22	1	US-08-379-078-697	Sequence 697, App
	21	22	1.4	22	3	US-09-339-775-4	Sequence 4, Appli
	22	22	1.4	22	4	US-07-974-409C-150	Sequence 150, App
	23	22	1.4	22	4	US-07-974-409C-164	Sequence 164, App
	24	22	1.4	22	4	US-07-974-409C-169	Sequence 169, App
	25	22	1.4	22	4	US-07-974-409C-211	Sequence 211, App
	26	22	1.4	22	4	US-07-974-409C-260	Sequence 260, App
	27	22	1.4	22	4	US-07-974-409C-261	Sequence 261, App
	28	22	1.4	22	4	US-07-974-409C-264	Sequence 264, App
	29	22	1.4	22	4	US-07-974-409C-265	Sequence 265, App
	30	22	1.4	22	4	US-07-974-409C-707	Sequence 707, App
	31	22	1.4	22	5	PCT-US93-00977-150	Sequence 150, App
	32	22	1.4	22	5	PCT-US93-00977-164	Sequence 164, App
	33	22	1.4	22	5	PCT-US93-00977-169	Sequence 169, App
	34	22	1.4	22	5	PCT-US93-00977-211	Sequence 211, App
	35	22	1.4	22	5	PCT-US93-00977-260	Sequence 260, App
	36	22	1.4	22	5	PCT-US93-00977-261	Sequence 261, App
	37	22	1.4	22	5	PCT-US93-00977-264	Sequence 264, App
	38	22	1.4	22	5	PCT-US93-00977-265	Sequence 265, App
	39	22	1.4	22	5	PCT-US93-00977-707	Sequence 707, App
c	40	21.8	1.4	25	4	US-09-827-998-1296	Sequence 1296, Ap
	41	21	1.4	21	1	US-08-379-078-566	Sequence 566, App
	42	21	1.4	21	1	US-08-379-078-577	Sequence 577, App
	43	21	1.4	21	1	US-08-379-078-582	Sequence 582, App
c	44	21	1.4	21	4	US-07-974-409C-144	Sequence 144, App
	45	21	1.4	21	4	US-07-974-409C-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-08-379-078-555
; Sequence 555, Application US/08379078
; Patent No. 5639612
; GENERAL INFORMATION:
; APPLICANT: Mitsuhashi, Masato
; APPLICANT: Cooper, Allan
; TITLE OF INVENTION: Gene Detection System
; NUMBER OF SEQUENCES: 726
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,078
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/974,406
; FILING DATE: 12-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.011CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 555:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-379-078-555

Query Match 1.7%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 2
US-08-379-078-560
; Sequence 560, Application US/08379078
; Patent No. 5639612
;  GENERAL INFORMATION:
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  Gene Detection System
;    NUMBER OF SEQUENCES:  726
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON AND BEAR
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,078
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/974,406
;      FILING DATE:  12-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  560:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-379-078-560

  Query Match             1.7%;  Score 26;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 3
US-08-379-078-665
; Sequence 665, Application US/08379078
; Patent No. 5639612
;  GENERAL INFORMATION:
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  Gene Detection System
;    NUMBER OF SEQUENCES:  726
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON AND BEAR
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,078
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/974,406
;      FILING DATE:  12-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  665:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-379-078-665

  Query Match             1.7%;  Score 26;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 4
US-07-974-409C-178
; Sequence 178, Application US/07974409C
; Patent No. 6300058
;  GENERAL INFORMATION:
;    APPLICANT:  Akitaya, Tatsuo
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  METHOD AND REAGENT
;    TITLE OF INVENTION:  FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  457
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/974,409C
;      FILING DATE:  12-NOV-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006CP2
```

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  178:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-974-409C-178

  Query Match             1.7%;  Score 26;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 5
US-07-974-409C-183
; Sequence 183, Application US/07974409C
; Patent No. 6300058
;  GENERAL INFORMATION:
;    APPLICANT:  Akitaya, Tatsuo
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  METHOD AND REAGENT
;    TITLE OF INVENTION:  FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  457
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/974,409C
;      FILING DATE:  12-NOV-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  183:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-974-409C-183

  Query Match             1.7%;  Score 26;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 6
US-07-974-409C-230
; Sequence 230, Application US/07974409C
; Patent No. 6300058
;  GENERAL INFORMATION:
;    APPLICANT:  Akitaya, Tatsuo
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  METHOD AND REAGENT
;    TITLE OF INVENTION:  FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  457
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/974,409C
;      FILING DATE:  12-NOV-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  230:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-974-409C-230

  Query Match             1.7%;  Score 26;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 7
PCT-US93-00977-178
; Sequence 178, Application PC/TUS9300977
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  711
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/00977
;       FILING DATE:  19930129
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Altman, Daniel E.
;       REGISTRATION NUMBER:  34,115
;       REFERENCE/DOCKET NUMBER:  HITACHI.006H
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  714-760-0404
;       TELEFAX:  714-760-9502
;   INFORMATION FOR SEQ ID NO:  178:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
PCT-US93-00977-178

  Query Match             1.7%;  Score 26;  DB 5;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 8
PCT-US93-00977-183
; Sequence 183, Application PC/TUS9300977
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  711
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00977
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006H
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  183:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US93-00977-183

  Query Match             1.7%;  Score 26;  DB 5;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 9
PCT-US93-00977-230
; Sequence 230, Application PC/TUS9300977
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  711
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00977
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006H
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  230:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US93-00977-230

  Query Match             1.7%;  Score 26;  DB 5;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3e+02;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        525 GATGTTCTTCGGACGAGAGTGAAGAC 550
              ||||||||||||||||||||||||||
Db          1 GATGTTCTTCGGACGAGAGTGAAGAC 26


RESULT 10
US-08-379-078-672
; Sequence 672, Application US/08379078
; Patent No. 5639612
;  GENERAL INFORMATION:
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  Gene Detection System
;    NUMBER OF SEQUENCES:  726
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON AND BEAR
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
```

```
;       COUNTRY:  USA
;       ZIP:  92660
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/379,078
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/974,406
;       FILING DATE:  12-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;       NAME:  Altman, Daniel E.
;       REGISTRATION NUMBER:  34,115
;       REFERENCE/DOCKET NUMBER:  HITACHI.011CP2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  714-760-0404
;       TELEFAX:  714-760-9502
;   INFORMATION FOR SEQ ID NO:  672:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  26 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
US-08-379-078-672

  Query Match             1.6%;  Score 24.4;  DB 1;  Length 26;
  Best Local Similarity   96.2%;  Pred. No. 8.3e+02;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        921 TGCCAGTTTGAAGATCTGAACAGAAG 946
              ||||||||| |||||||||||||||| ||||
Db          1 TGCCAGTTTGAAGATCTGAACCGAAG 26


RESULT 11
US-07-974-409C-231
; Sequence 231, Application US/07974409C
; Patent No. 6300058
;  GENERAL INFORMATION:
;    APPLICANT:  Akitaya, Tatsuo
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  METHOD AND REAGENT
;    TITLE OF INVENTION:  FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  457
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/974,409C
;      FILING DATE:  12-NOV-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  231:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-974-409C-231

  Query Match             1.6%;  Score 24.4;  DB 4;  Length 26;
  Best Local Similarity   96.2%;  Pred. No. 8.3e+02;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        921 TGCCAGTTTGAAGATCTGAACAGAAG 946
              |||||||||||||||||||| ||||
Db          1 TGCCAGTTTGAAGATCTGAACCGAAG 26


RESULT 12
PCT-US93-00977-231
; Sequence 231, Application PC/TUS9300977
;  GENERAL INFORMATION:
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;    NUMBER OF SEQUENCES:  711
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson, and Bear
;      STREET:  620 Newport Center Dr.  Sixteenth Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/00977
;      FILING DATE:  19930129
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI.006H
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  231:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US93-00977-231

  Query Match             1.6%;  Score 24.4;  DB 5;  Length 26;
  Best Local Similarity   96.2%;  Pred. No. 8.3e+02;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        921 TGCCAGTTTGAAGATCTGAACAGAAG 946
              |||||||||||||||||||| ||||
Db          1 TGCCAGTTTGAAGATCTGAACCGAAG 26


RESULT 13
US-09-339-775-2
```

```
; Sequence 2, Application US/09339775
; Patent No. 6063626
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-I3 EXPRESSION
;  FILE REFERENCE: RTS-0069
;  CURRENT APPLICATION NUMBER: US/09/339,775
;  CURRENT FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 2
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Primer
US-09-339-775-2

  Query Match             1.5%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        273 GGACGGCTAAAGATTGACTTTGG 295
              |||||||||||||||||||||||
Db          1 GGACGGCTAAAGATTGACTTTGG 23


RESULT 14
US-09-339-775-3/c
; Sequence 3, Application US/09339775
; Patent No. 6063626
; GENERAL INFORMATION:
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-I3 EXPRESSION
;  FILE REFERENCE: RTS-0069
;  CURRENT APPLICATION NUMBER: US/09/339,775
;  CURRENT FILING DATE: 1999-06-24
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: PCR Primer
US-09-339-775-3

  Query Match             1.5%;  Score 23;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        329 ATTTGTTTTAGCTGGCAGTGCTG 351
              |||||||||||||||||||||||
Db         23 ATTTGTTTTAGCTGGCAGTGCTG 1


RESULT 15
US-08-379-078-527
; Sequence 527, Application US/08379078
; Patent No. 5639612
;  GENERAL INFORMATION:
;    APPLICANT:  Mitsuhashi, Masato
;    APPLICANT:  Cooper, Allan
;    TITLE OF INVENTION:  Gene Detection System
;    NUMBER OF SEQUENCES:  726
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KNOBBE, MARTENS, OLSON AND BEAR
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/379,078
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/974,406
;      FILING DATE:  12-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Altman, Daniel E.
;      REGISTRATION NUMBER:  34,115
;      REFERENCE/DOCKET NUMBER:  HITACHI:011CP2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  714-760-0404
;      TELEFAX:  714-760-9502
;  INFORMATION FOR SEQ ID NO:  527:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-379-078-527

  Query Match             1.4%;  Score 22;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 AGCACCATTGTGAAACAGATGA 168
              ||||||||||||||||||||||
Db          1 AGCACCATTGTGAAACAGATGA 22


Search completed: September 14, 2004, 16:52:04
Job time : 145 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 14:03:51 ; Search time 761 Seconds
(without alignments)
10201.892 Million cell updates/sec

Title: US-10-018-497A-1
Perfect score: 1543
Sequence: 1 gaattcggatgggctgcacg.....tgaaaaaaaaagccgaattc 1543

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26.8	1.7	30	17	US-10-718-948-31	Sequence 31, Appl
2	25.8	1.7	29	17	US-10-718-948-33	Sequence 33, Appl
3	24.2	1.6	29	13	US-10-157-073-204	Sequence 204, App
4	24.2	1.6	29	13	US-10-157-106A-204	Sequence 204, App
5	24.2	1.6	29	13	US-10-157-171-204	Sequence 204, App
6	24.2	1.6	29	13	US-10-157-491-204	Sequence 204, App
7	24.2	1.6	29	13	US-10-156-792A-204	Sequence 204, App
8	24.2	1.6	29	13	US-10-157-178-204	Sequence 204, App
9	24.2	1.6	29	13	US-10-157-213-204	Sequence 204, App
10	24.2	1.6	29	15	US-10-157-305A-204	Sequence 204, App
11	24.2	1.6	29	15	US-10-157-391-204	Sequence 204, App
12	24.2	1.6	29	15	US-10-157-096-204	Sequence 204, App
13	24.2	1.6	29	15	US-10-157-302-204	Sequence 204, App
14	24.2	1.6	29	15	US-10-157-215A-204	Sequence 204, App
15	24.2	1.6	29	15	US-10-157-299-204	Sequence 204, App
16	24.2	1.6	29	15	US-10-154-951B-204	Sequence 204, App
17	24.2	1.6	29	15	US-10-156-831-204	Sequence 204, App
18	24.2	1.6	29	15	US-10-157-147-204	Sequence 204, App
19	24.2	1.6	29	15	US-10-157-166-204	Sequence 204, App
20	24.2	1.6	29	15	US-10-156-902-204	Sequence 204, App
21	24.2	1.6	29	15	US-10-157-318-204	Sequence 204, App
22	24.2	1.6	29	16	US-10-156-811-204	Sequence 204, App
23	24.2	1.6	29	16	US-10-157-320A-204	Sequence 204, App
24	24.2	1.6	29	16	US-10-157-418A-204	Sequence 204, App
25	24.2	1.6	29	16	US-10-157-317-204	Sequence 204, App
26	24.2	1.6	29	16	US-10-157-339-204	Sequence 204, App
27	23.2	1.5	28	17	US-10-718-948-30	Sequence 30, Appl
c 28	22	1.4	30	13	US-10-157-073-205	Sequence 205, App
c 29	22	1.4	30	13	US-10-157-106A-205	Sequence 205, App
c 30	22	1.4	30	13	US-10-157-171-205	Sequence 205, App
c 31	22	1.4	30	13	US-10-157-491-205	Sequence 205, App
c 32	22	1.4	30	13	US-10-156-792A-205	Sequence 205, App
c 33	22	1.4	30	13	US-10-157-178-205	Sequence 205, App
c 34	22	1.4	30	13	US-10-157-213-205	Sequence 205, App
c 35	22	1.4	30	15	US-10-157-305A-205	Sequence 205, App
c 36	22	1.4	30	15	US-10-157-391-205	Sequence 205, App
c 37	22	1.4	30	15	US-10-157-096-205	Sequence 205, App
c 38	22	1.4	30	15	US-10-157-302-205	Sequence 205, App
c 39	22	1.4	30	15	US-10-157-215A-205	Sequence 205, App
c 40	22	1.4	30	15	US-10-157-299-205	Sequence 205, App
c 41	22	1.4	30	15	US-10-154-951B-205	Sequence 205, App
c 42	22	1.4	30	15	US-10-156-831-205	Sequence 205, App
c 43	22	1.4	30	15	US-10-157-147-205	Sequence 205, App
c 44	22	1.4	30	15	US-10-157-166-205	Sequence 205, App
c 45	22	1.4	30	15	US-10-156-902-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-10-718-948-31
; Sequence 31, Application US/10718948
; Publication No. US20040127575A1
; GENERAL INFORMATION:
; APPLICANT: Feng, Ying
; APPLICANT: Higgings, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: US/10/718,948
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/504585
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-718-948-31

Query Match 1.7%; Score 26.8; DB 17; Length 30;
Best Local Similarity 93.3%; Pred. No. 5.2e+03;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        462 GCTTCATATTATCTAAATGATCTGGATAGA 491
              |||||||||||  |||||||||  ||||||||
Db          1 GCTTCATATTACCTAAATGATTTGGATAGA 30
```

RESULT 2
US-10-718-948-33
; Sequence 33, Application US/10718948
; Publication No. US20040127575A1
; GENERAL INFORMATION:
; APPLICANT: Feng, Ying
; APPLICANT: Higgings, Linda
; APPLICANT: Kapoun, Ann
; APPLICANT: Liu, David
; APPLICANT: Schreiner, George
; TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
; TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
; FILE REFERENCE: 39739-0029
; CURRENT APPLICATION NUMBER: US/10/718,948
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/504585
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/429046
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-718-948-33

Query Match 1.7%; Score 25.8; DB 17; Length 29;
Best Local Similarity 93.1%; Pred. No. 9.2e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        495 TCCCAGTCTAACTACATTCCAACTCAGCA 523
              |||||| | ||||||||||||||||||||
Db          1 TCCCAGACCAACTACATTCCAACTCAGCA 29
```

RESULT 3
US-10-157-073-204
; Sequence 204, Application US/10157073
; Publication No. US20030211086A1
; GENERAL INFORMATION:
; APPLICANT: Neil Berkley
; APPLICANT: Sabbadini, Roger A.
; TITLE OF INVENTION: MINICELL-BASED SELECTIVE ABSORPTION
; FILE REFERENCE: MPEX.008DV24
; CURRENT APPLICATION NUMBER: US/10/157,073
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-073-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 4
US-10-157-106A-204
; Sequence 204, Application US/10157106A
; Publication No. US20030211599A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Klepper, Robert
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED DELIVERY AGENTS
; FILE REFERENCE: MPEX.008DV5
; CURRENT APPLICATION NUMBER: US/10/157,106A
; CURRENT FILING DATE: 2020-05-28
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-106A-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 5
US-10-157-171-204
; Sequence 204, Application US/10157171
; Publication No. US20030224369A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; APPLICANT: William Gerhart
; TITLE OF INVENTION: REVERSE SCREENING AND TARGET
; TITLE OF INVENTION: IDENTIFICATION WITH MINICELLS
; FILE REFERENCE: MPEX.008DV18
; CURRENT APPLICATION NUMBER: US/10/157,171
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-171-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
```

```
                  ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 6
US-10-157-491-204
; Sequence 204, Application US/10157491
; Publication No. US20030224444A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; APPLICANT: Mark W. Surber
; TITLE OF INVENTION: ANTIBODIES TO NATIVE CONFORMATIONS OF
; TITLE OF INVENTION: MEMBRANE PROTEINS
; FILE REFERENCE: MPEX.00813
; CURRENT APPLICATION NUMBER: US/10/157,491
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-491-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 7
US-10-156-792A-204
; Sequence 204, Application US/10156792A
; Publication No. US20030203411A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Berkley, Neil
; APPLICANT: Klepper, Robert
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: METHODS OF MINICELL-BASED DELIVERY
; FILE REFERENCE: MPEX.008DV6
; CURRENT APPLICATION NUMBER: US/10/156,792A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-156-792A-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 8
US-10-157-178-204
; Sequence 204, Application US/10157178
; Publication No. US20030202937A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Robert Klepper
; APPLICANT: Neil Berkley
; TITLE OF INVENTION: MINICELL-BASED DIAGNOSTICS
; FILE REFERENCE: MPEX.008DV11
; CURRENT APPLICATION NUMBER: US/10/157,178
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-178-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 9
US-10-157-213-204
; Sequence 204, Application US/10157213
; Publication No. US20030203481A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Klepper, Robert
; TITLE OF INVENTION: CONJUGATED MINICELLS
; FILE REFERENCE: MPEX.008DV7
; CURRENT APPLICATION NUMBER: US/10/157,213
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-213-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 10
US-10-157-305A-204
; Sequence 204, Application US/10157305A
; Publication No. US20030166099A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; APPLICANT: Anca M. Segall
; APPLICANT: Robert Klepper
; TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
; FILE REFERENCE: MPEX.008DV1
; CURRENT APPLICATION NUMBER: US/10/157,305A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-305A-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 11
US-10-157-391-204
; Sequence 204, Application US/10157391
; Publication No. US20030166279A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
; FILE REFERENCE: MPEX.008DV14
; CURRENT APPLICATION NUMBER: US/10/157,391
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-391-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 12
US-10-157-096-204
; Sequence 204, Application US/10157096
; Publication No. US20030190601A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: TARGET DISPLAY ON MINICELLS
; FILE REFERENCE: MPEX.008DV12
; CURRENT APPLICATION NUMBER: US/10/157,096
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,51
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-096-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 13
US-10-157-302-204
; Sequence 204, Application US/10157302
; Publication No. US20030190683A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED RATIONAL DRUG DESIGN
; FILE REFERENCE: MPEX.008DV17
; CURRENT APPLICATION NUMBER: US/10/157,302
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-302-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 14
US-10-157-215A-204
; Sequence 204, Application US/10157215A
; Publication No. US20030190749A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Segall, Anca M.
; APPLICANT: Berkley, Neil
; TITLE OF INVENTION: MINICELL-PRODUCING PARENT CELLS
; FILE REFERENCE: MPEX.008DV23
; CURRENT APPLICATION NUMBER: US/10/157,215A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-215A-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

RESULT 15
US-10-157-299-204
; Sequence 204, Application US/10157299
; Publication No. US20030194714A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED TRANSFORMATION
; FILE REFERENCE: MPEX.008DV15
; CURRENT APPLICATION NUMBER: US/10/157,299
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer

US-10-157-299-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy         11 GGGCTGCACGTTGAGCGCCGAAGACAAGG 39
              ||||||||| |||||||||| |||||||
Db          1 GGGCTGCACCGTGAGCGCCGAGGACAAGG 29
```

Search completed: September 14, 2004, 17:04:52
Job time : 762 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 13:57:38 ; Search time 3736 Seconds
(without alignments)
12333.336 Million cell updates/sec

Title: US-10-018-497A-1
Perfect score: 1543
Sequence: 1 gaattcggatgggctgcacg.....tgaaaaaaaaagccgaattc 1543

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 38748

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	19.2	1.2	29	29	TA224C08P	AL480654 T. brucei
c	2	18.8	1.2	30	28	AZ650939	AZ650939 1M0521D19
c	3	17.6	1.1	28	14	CF305214	CF305214 CLD1--01-
c	4	17.4	1.1	30	9	AU264114	AU264114 AU264114
	5	17	1.1	26	14	D18738	D18738 MUSGS01800
	6	17	1.1	28	14	CF305384	CF305384 CLD1--01-
c	7	16.8	1.1	25	14	D11538	D11538 HUM0C12B03
c	8	16.6	1.1	26	13	BQ584385	BQ584385 E011858-0
c	9	16.6	1.1	27	28	BZ358395	BZ358395 SALK_1324
c	10	16.4	1.1	20	28	AZ462631	AZ462631 1M0269F12
c	11	16.4	1.1	26	28	AZ581086	AZ581086 1M0369E11
c	12	16.4	1.1	30	13	C20896	C20896 HUMGS000497
	13	16.4	1.1	30	14	CF319624	CF319624 HD--10-D0
c	14	16.2	1.0	27	9	AV739265	AV739265 AV739265
c	15	16.2	1.0	29	28	AZ827011	AZ827011 2M0103I12
	16	16.2	1.0	30	9	AU257497	AU257497 AU257497
	17	16.2	1.0	30	9	AU267300	AU267300 AU267300
c	18	16.2	1.0	30	13	C00680	C00680 HUMGS000823
c	19	16.2	1.0	30	28	AZ773045	AZ773045 1M0584A23
	20	16	1.0	23	28	AZ345757	AZ345757 1M0080A10
c	21	16	1.0	27	28	AZ442586	AZ442586 1M0236M18
c	22	16	1.0	28	10	AW246684	AW246684 2822003.3
c	23	15.8	1.0	24	14	D11965	D11965 HUM000S128
c	24	15.8	1.0	24	14	D12217	D12217 HUM000S358
c	25	15.8	1.0	25	9	AW059699	AW059699 AHuTH.bss
c	26	15.8	1.0	28	14	D12304	D12304 HUM000S518
c	27	15.8	1.0	28	14	D12462	D12462 HUM00TW404
c	28	15.8	1.0	28	14	D12466	D12466 HUM00TW469
	29	15.8	1.0	29	28	AZ433903	AZ433903 1M0220G03
c	30	15.8	1.0	30	9	AL048690	AL048690 DKFZp566D
	31	15.8	1.0	30	28	AZ583194	AZ583194 1M0378A08
	32	15.6	1.0	25	14	CF319499	CF319499 HD--10-A1
	33	15.6	1.0	28	9	AI800173	AI800173 tr23d08.x
	34	15.6	1.0	28	28	AZ824122	AZ824122 2M0098M01
	35	15.6	1.0	29	28	AZ579541	AZ579541 1M0367I08
	36	15.6	1.0	29	28	AZ806533	AZ806533 2M0068H09
	37	15.6	1.0	30	10	AW248759	AW248759 2820825.3
	38	15.6	1.0	30	14	D18724	D18724 MUSGS01786
c	39	15.6	1.0	30	28	AZ458127	AZ458127 1M0261I24
c	40	15.4	1.0	25	28	AZ625569	AZ625569 1M0465I12
c	41	15.4	1.0	25	28	BZ769654	BZ769654 SALK_1425
c	42	15.4	1.0	25	29	TA12F02Q	AL451366 T. brucei
	43	15.4	1.0	26	10	AW246553	AW246553 2822092.3
	44	15.4	1.0	26	28	AZ432649	AZ432649 1M0218H11
	45	15.4	1.0	27	14	CF333518	CF333518 JMT--02-H

ALIGNMENTS

RESULT 1
TA224C08P/c
LOCUS TA224C08P 29 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 224c08, forward sequence, genomic survey sequence.
ACCESSION AL480654
VERSION AL480654.1 GI:11846423
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 29)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small

insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES Location/Qualifiers
source 1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="224c08"

ORIGIN

Query Match 1.2%; Score 19.2; DB 29; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+07;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1388 TTACTCTTTTTTTCCCCCCTTCTT 1411
|| | ||||||||||||||||||||
Db 29 TTTTTTTTTTTTCCCCCCTTCTT 6

RESULT 2
AZ650939/c
LOCUS AZ650939 30 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0521D19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0521D19 F, genomic survey sequence.
ACCESSION AZ650939
VERSION AZ650939.1 GI:11785931
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 30)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0521 row: D column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 30.

FEATURES Location/Qualifiers
source 1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0521D19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.2%; Score 18.8; DB 28; Length 30;
Best Local Similarity 76.7%; Pred. No. 1.7e+07;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 743 AAGCATGAAACTGTTTGACAGCATTTGTAA 772
|||| ||| | |||||| ||||||| ||
Db 30 AAGCCTGACAGTGTTTGTGAGCATTTACAA 1

RESULT 3
CF305214/c
LOCUS CF305214 28 bp mRNA linear EST 15-AUG-2003
DEFINITION CLD1--01-B13.b1 Rice cold treated leaf plasmid cDNA library (CLD1) Oryza sativa cDNA clone CLD1--01-B13, mRNA sequence.
ACCESSION CF305214
VERSION CF305214.1 GI:33676975
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers
source 1. .28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="CLD1--01-B13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

ORIGIN

Query Match 1.1%; Score 17.6; DB 14; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.1e+07;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1388 TTACTCTTTTTTTCCCCCCTTCTT 1411
|| |||||||||||||| | || ||
Db 28 TTCCTCTTTTTTTCCCTCTTTTTT 5

```
RESULT 4
AU264114/c
LOCUS       AU264114                  30 bp    mRNA    linear   EST 10-MAY-2002
DEFINITION  AU264114 VS Dictyostelium discoideum cDNA clone VSD485 5', mRNA
            sequence.
ACCESSION   AU264114
VERSION     AU264114.1  GI:20522912
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum
  ORGANISM  Dictyostelium discoideum
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
            Takeuchi,I., Kohara,Y. and Tanaka,Y.
  TITLE     Population analysis of cDNAs from unicellular and multicellular
            stages of Dictyostelium discoideum
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hideko Urushihara
            Institute of Biological Sciences
            University of Tsukuba
            1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
            Tel: 81-298-53-4664
            Fax: 81-298-53-6614
            Email: hideko@biol.tsukuba.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Dictyostelium discoideum"
                     /mol_type="mRNA"
                     /strain="AX4"
                     /db_xref="taxon:44689"
                     /clone="VSD485"
                     /sex="mat A"
                     /dev_stage="vegetative"
                     /clone_lib="VS"
ORIGIN

  Query Match             1.1%;  Score 17.4;  DB 9;  Length 30;
  Best Local Similarity   77.8%;  Pred. No. 3.4e+07;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1477 TTCTTTATTTGCAAAAGAATCTTTATT 1503
              || ||| ||| ||||| |||  |||||
Db         30 TTTTTTTTTTCCAAAAAAATAATTATT 4


RESULT 5
D18738
LOCUS       D18738                    26 bp    mRNA    linear   EST 12-DEC-1995
DEFINITION  MUSGS01800 Mouse 3'-directed Mus musculus domesticus cDNA clone
            md1688 3', mRNA sequence.
ACCESSION   D18738
VERSION     D18738.1  GI:1100707
KEYWORDS    EST.
SOURCE      Mus musculus domesticus (western European house mouse)
  ORGANISM  Mus musculus domesticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
  TITLE     Analysis of gene expression in mouse embryogenesis by 3'-directed
            cDNA sequencing
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and
            Matsubara,K.
            Institute for Cellular and Molecular Biology
            Osaka University
            3-1 Yamada-oka, Suita, Osaka 565, Japan.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus musculus domesticus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /sub_species="domesticus"
                     /db_xref="taxon:10092"
                     /clone="md1688"
                     /tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
                     /clone_lib="Mouse 3'-directed"
ORIGIN

  Query Match             1.1%;  Score 17;  DB 14;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 4.2e+07;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        137 ATCTGGTAAAAGCACCATTGTGAAA 161
              ||||| |||||  ||||||  ||||
Db          2 ATCTGATAAAATAACCATTTGGAAA 26


RESULT 6
CF305384
LOCUS       CF305384                  28 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  CLD1--01-J01.b1 Rice cold treated leaf plasmid cDNA library (CLD1)
            Oryza sativa cDNA clone CLD1--01-J01, mRNA sequence.
ACCESSION   CF305384
VERSION     CF305384.1  GI:33677145
KEYWORDS    EST.
SOURCE      Oryza sativa
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="CLD1--01-J01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice cold treated leaf plasmid cDNA library
                     (CLD1)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was
                     incubated at 4 C(360uM/m-2sec-1) for 2hrs. Oligo-capped
                     mRNA was reverse transcribed and then used for PCR."
ORIGIN

  Query Match             1.1%;  Score 17;  DB 14;  Length 28;
  Best Local Similarity   80.0%;  Pred. No. 4.2e+07;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        826 TTTTTGAGGAAAAAATAAAGAGGAG 850
              |||||| | |||||| ||| ||| |
Db          2 TTTTTGGGAAAAAAAAAAAAAGGCG 26


RESULT 7
D11538/c
LOCUS       D11538                    25 bp    mRNA    linear   EST 02-DEC-1992
DEFINITION  HUM0C12B03 Liver HepG2 cell line. Homo sapiens cDNA clone c12b03,
            mRNA sequence.
```

```
ACCESSION   D11538
VERSION     D11538.1  GI:2148686
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima,A., Kojima,Y.
            and Matsubara,K.
  TITLE     Large scale cDNA sequencing for analysis of quantitative and
            qualitative aspects of gene expression
  JOURNAL   Nat. Genet. 2, 173-179 (1992)
  MEDLINE   94258199
   PUBMED   1345164
COMMENT     Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
            Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
            Institute for Molecular and Cellular Biology
            Osaka University
            1-3 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:D0S8040E"
                     /db_xref="taxon:9606"
                     /clone="c12b03"
                     /lab_host="E.coli"
                     /clone_lib="Liver HepG2 cell line."
                     /note="3'-directed regional cDNA library. Cleaved by MboI
                     and transformed into E.coli."
ORIGIN

  Query Match           1.1%;  Score 16.8;  DB 14;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 4.7e+07;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1468 AAATTTTATTTCTTTATTTG 1487
              ||||||||| |||||||||
Db         23 AAATTTTATAACTTTATTTG 4


RESULT 8
BQ584385/c
LOCUS       BQ584385                 26 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E011858-024-003-A19-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-003-A19 5-PRIME, mRNA sequence.
ACCESSION   BQ584385
VERSION     BQ584385.1  GI:26113962
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 26   Std Error: 0.00
            Plate: 3  row: A  column: 19
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:182321"
                     /db_xref="taxon:161934"
                     /clone="024-003-A19"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match           1.1%;  Score 16.6;  DB 13;  Length 26;
  Best Local Similarity   82.6%;  Pred. No. 5.2e+07;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       770 TAATAACAAATGGTTTACAGAAA 792
             || |||| | |||||||||| |||
Db        23 TATTAACGATTGGTTTACAAAAA 1


RESULT 9
BZ358395/c
LOCUS       BZ358395                 27 bp    DNA     linear   GSS 14-NOV-2002
DEFINITION  SALK_132488.23.30.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_132488.23.30.x, genomic
            survey sequence.
ACCESSION   BZ358395
VERSION     BZ358395.1  GI:24950657
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_132488.23.30.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
```

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 1.1%; Score 16.6; DB 28; Length 27;
Best Local Similarity 82.6%; Pred. No. 5.2e+07;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       1470 ATTTTATTTCTTTATTTGCAAAA 1492
              | || | || ||||||||||||||
Db         27 AATTCAATTATTTATTTGCAAAA 5
```

RESULT 10
AZ462631/c
LOCUS AZ462631 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0269F12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0269F12 R, genomic survey sequence.
ACCESSION AZ462631
VERSION AZ462631.1 GI:10620672
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: F column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0269F12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.1%; Score 16.4; DB 28; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.8e+07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1426 TCATTTTTAAGGTTTTTT 1443
              |||||||| |||||||||
Db         18 TCATTTTTCAGGTTTTTT 1
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RESULT 11
AZ581086/c
LOCUS AZ581086 26 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0369E11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0369E11 R, genomic survey sequence.
ACCESSION AZ581086
VERSION AZ581086.1 GI:11695746
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
FEATURES Location/Qualifiers
source 1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0369E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 1.1%; Score 16.4; DB 28; Length 26;
Best Local Similarity 76.9%; Pred. No. 5.7e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1364 GCATTCTAGAACTTCATATGTAGCTT 1389
||||| |||||||| | |||| ||
Db 26 GCATTGTAGAACTTAGTGGGTAGATT 1

RESULT 12
C20896/c
LOCUS C20896 30 bp mRNA linear EST 31-DEC-2002
DEFINITION HUMGS0004970 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA sequence.
ACCESSION C20896
VERSION C20896.1 GI:1622006
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 30)
AUTHORS Okubo,K.
TITLE BodyMap; human gene expression database
JOURNAL Unpublished (1995)
COMMENT Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see ' http://www.imcb.osaka- u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.
FEATURES Location/Qualifiers
source 1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
ORIGIN

Query Match 1.1%; Score 16.4; DB 13; Length 30;
Best Local Similarity 76.9%; Pred. No. 5.6e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1491 AAGAATCTTTATTAAAACAAACAATC 1516
|| || |||| |||||||||| |||
Db 26 AATTATTTTTAATAAAACAAAAGATC 1

RESULT 13
CF319624
LOCUS CF319624 30 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--10-D06.b1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.
ACCESSION CF319624
VERSION CF319624.1 GI:33691385
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES Location/Qualifiers
source 1. .30
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
ORIGIN

Query Match 1.1%; Score 16.4; DB 14; Length 30;
Best Local Similarity 76.9%; Pred. No. 5.6e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1471 TTTTATTTCTTTATTTGCAAAAGAAT 1496
|||| ||| ||||| | |||||| |
Db 5 TTTTTTTTTTTTATAGGAAAAAGAGT 30

RESULT 14
AV739265/c
LOCUS AV739265 27 bp mRNA linear EST 17-OCT-2000
DEFINITION AV739265 CB Homo sapiens cDNA clone CBFAWE01 5', mRNA sequence.
ACCESSION AV739265
VERSION AV739265.1 GI:10856846
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 27)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
FEATURES Location/Qualifiers
source 1. .27
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="CBFAWE01"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/note="Vector: pBluescript; Site_1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

ORIGIN

Query Match 1.0%; Score 16.2; DB 9; Length 27;
Best Local Similarity 78.3%; Pred. No. 6.3e+07;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       1388 TTACTCTTTTTTTCCCCCCTTCT 1410
              ||  | ||||||  | ||||||||
Db         24 TTTTTTTTTTTTNCNCCCCTTCT 2
```

RESULT 15
AZ827011/c
LOCUS AZ827011 29 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0103I12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103I12 F, genomic survey sequence.
ACCESSION AZ827011
VERSION AZ827011.1 GI:12996919
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: I column: 12
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES Location/Qualifiers
source 1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103I12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.0%; Score 16.2; DB 28; Length 29;
Best Local Similarity 72.4%; Pred. No. 6.2e+07;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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